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LOCUS      ATH243015          5000 bp      DNA      linear      PLN 01-JUN-2001
DEFINITION Arabidopsis thaliana LGT1 gene, and partial FUSCA6 gene.
ACCESSION  AJ243015
VERSION    AJ243015.1   GI:7799776
KEYWORDS   FUSCA6 gene; FUSCA6 protein; LGT1 gene; like glycosyl transferase
           1.
SOURCE     Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1
  AUTHORS  Tavares,R., Aubourg,S., Lecharny,A. and Kreis,M.
  TITLE    Organization and structural evolution of four multigene families in
           Arabidopsis thaliana: AtLCAD, AtLGT, AtMYST and AtHD-GL2
  JOURNAL  Plant Mol. Biol. 42 (5), 703-717 (2000)
  PUBMED   10809443
REFERENCE  2 (bases 1 to 5000)
  AUTHORS  Tavares,R.
  TITLE    Direct Submission
  JOURNAL  Submitted (07-MAY-1999) R. Tavares, Institut de Biotechnologie des
           Plantes, Biologie du Developpement des Plantes, Universite
           Paris-Sud, Batiment 630, F-91405 Orsay Cedex, FRANCE
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## ORIGIN

## Alignment Scores:

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Best Local Similarity:	64.5%	Mismatches:	3
Query Match:	90.5%	Indels:	369
DB:	4	Gaps:	9

US-10-544-180A-2 (1-673) x ATH243015 (1-5000)

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Qy          50 ----- 50

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Qy          50 ----- 50

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Qy          50 ----- 50

Db          930 CTTGATGTGACACTGATGATATTCAGACAATTGCTATTTTTCTAGACTGGCAAAATTGGT 989

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Qy	109	ArgGlyThrGlyValAspProSerPheArgHisSerGlu-----	121
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Qy	122	-----AsnProAlaThrProAspValLysSerAsnAsnLeuAsnGluLysArgAsp	138
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Qy	139	SerIleSerLys-----	142
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Qy	143	-----AspSerIleHisGlnLysValGluThrPro	152
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Qy	159	-----GlnLeuArgGluLysArgArgGluMetArgAlaAsnGluLeuValGln	174
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Qy	175	HisAsnAspAspThrIleLeuLysLeuGluAsnAlaAlaIleGluArgSerLysSerVal	194
Db	1948	CACAATGATGACACGATTTTGAACTCGAAAATGCTGCCATTGAACGCTCTAAGTCTGTT	2007

Qy	195	AspSerAlaValLeuGlyLysTyrSerIleTrpArgArgGluAsnGluAsnAspAsnSer	214
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Qy	235	AlaLysLeuLysAsnLysAsnAspLeuLeuGlnGluLeuGlnAlaArgLeuLysAspSer	254
Db	2128	GCAAAATTGAAAAACAAGAACGATTTGTTACAAGAACTCCAGGCCCGACTTAAGGACAGC	2187
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Qy	324	AlaAlaLysThrIleProAsnProIleHisCysLeuSerMetArgLeuThrIleAspTyr	343
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Qy	344	TyrLeuLeuSerProGluLysArgLysPheProArgSerGluAsnLeuGluAsnProAsn	363
Db	2548	TATCTTCTGTCTCCGGAGAAAAGAAAATTCCTCGGAGTGAAACCTAGAAAACCTAAT	2607
Qy	364	LeuTyrHisTyrAlaLeuPheSerAspAsnValLeuAlaAlaSerValValValAsnSer	383
Db	2608	CTTTATCATTATGCCCTCTTTTCCGACAATGTATTAGCTGCATCAGTAGTTGTAACTCA	2667
Qy	384	ThrIleMetAsnAlaLys-----	389
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Db	2787	TATGTGCAGGATCCTTCTAAGCATGTTTTTCACCTTGTCACGGATAAACTCAATTTCGGA	2846
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Db	2847	GCAATGAACATGTGGTTCCTCCTAAACCCACCCGAAAGGCAACCATACATGTGGAAAAC	2906
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Qy      467  LysTyrArgAsnProLysTyrLeuSerMetLeuAsnHisLeuArgPheTyrLeuProGlu 486
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